PART IV: ANTIBODY BINDING SITES

How to Use Part IV: Monoclonal Antibody Index (MAb), Anti-HIV Antibody Tables, and Maps

This section summarizes HIV-specific antibodies arranged sequentially according to the location of their binding domain, organized by protein. We attempted to make this section as comprehensive as possible. For the MAbs capable of binding to linear peptides, we require that the binding site be contained within a region of 30 or so amino acids, but not that the precise boundaries be defined. MAbs that cannot bind to linear peptides are grouped by category at the end of each protein. Antibody categories, for example CD4BS antibodies, are noted in the index at the beginning of this section. Studies of polyclonal Ab esponses are also included. Responses that are just characterized by binding to a protein, with no know specific binding site, are listed at the end of each protein. For more recent updates, epitope sequence alignments, and search capabilities, please see our web site: http://hiv-web.lanl.gov/immunology.

A. INDICES

Two indices are provided. The first lists the MAb's IDs in alphabetical order so one can find their location in the table. The second provides a concise list of the MAbs in order of their appearance in the antibody table, *i.e.*, ordered by the protein coding regions spanning HIV-1.

B. TABLES:

Each MAb has an nine-part basic entry:
- **Number:** Order of appearance in this table.
- **MAb ID:** The name of the monoclonal antibody with synonyms in parentheses. MAbs often have several names. For example, punctuation can be lost and names are often shortened (M-70 in one paper can be M70 in another). Polyclonal responses are listed as "polyclonal" in this field.
- **HXB2 Location:** Position of the binding site on the viral strain HXB2, which is used as a reference strain throughout this publication. The numbering corresponds to the protein maps. Because of HIV-1 variation the epitope may not actually be present in HXB2, and the position in HXB2 indicates the position aligned to the epitope.
- **Author Location:** The amino acid positions of the epitope boundaries and the reference sequence are listed as given in the primary publication.

Frequently, these positions as published are imprecise, and do not truly correspond to the numbering of the sequence, but they provide a reasonable guide to the peptide's approximate location in the protein. Also, in many cases, reference sequence identification was not provided; because of HIV-1's variability, position numbers require a reference strain to be meaningful. Binding sites that cannot be defined through peptide binding or interference studies are labeled as discontinuous. The approximate location on the protein, sequence number, and reference sequence are listed. If you are interested in finding the precise positions of an antigen you are studying on the HXB2 reference strain, please try using the interactive position locator at our web site: http://hiv-web.lanl.gov/NUM-HXB2/HXB2.MAIN.html.

- **Sequence:** The amino acid sequence of the binding region of interest, based on the reference strain used in the study defining the binding site. On rare occasions, when only the position numbers and not the actual peptide sequence was specified in the original publication, if the sequences were numbered inaccurately by the primary authors, we may have misrepresented the binding site's amino acid sequence. Therefore, epitopes that were not explicitly written in the primary publication, that we determined by looking up the reference strain and the numbered location, are followed by a question mark in the table.
- **Neutralizing: L**: neutralizes lab strains. **P**: neutralizes primary isolates. **no**: does not neutralize.
- **Immunogen:** The antigenic stimulus of the original B cell response. If a vaccine was used as the original antigenic stimulation, not a natural infection, this is noted on a separate line, and additional information about the vaccine antigen is provided as available.
- **Species(Isotype):** The host that the antibody was generated in, and the isotype of the antibody.
- **References:** All publications that we could find that refer to the use of a specific monoclonal antibody. First is a list of all references. Second is a list of the donors, and is meant to serve as a potential guide to a source of information about an antibody or how to obtain it, as well as to provide credit. Then comes a list of notes describing the context of each study, and what was learned about the antibody in the study.

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C. MAPS

The names of MAbs and the location of well characterized linear binding sites of 21 amino acids or less are indicated on protein sequences of the HXB2 clone. This map is meant to provide the relative location of epitopes on a given protein, but the HXB2 sequence may not actually bind to the MAb of interest, as it may vary relative to the sequence for which the epitope was defined. HXB2 was selected as the reference strain because so many studies use HXB2, and because crystal structures for HXB2-related proteins are often available.

ALIGNMENTS

Alignments that correspond to the epitopes are only available from the web site, not in this book, because of space limitations. All epitopes are aligned to the HXB2 sequence, with the sequence used to define the epitope indicated directly above it. In consensus sequences an upper case letter indicates the amino acid was present in all sequences, a lower case letter indicates the amino acid was present in most sequences in a given position, and a question mark indicates two or more amino acids were represented with equal frequency.

The master alignment files from which the epitope alignments were created are available at our web site (`http://hiv-web.lanl.gov/ALIGN_CURRENT/ALIGN-INDEX.html`), and we restricted ourselves to full protein sequences for these alignments, excluding short fragments of sequences. The subtype designation and the country of isolation are indicated along with the common name of the sequence. The alignments were modified in some cases to optimize the alignment relative to the defined epitope and minimize insertions and deletions; epitope alignments are generated by anchoring on the C-terminal residue. A dash indicates identity to the consensus sequence, and a period indicates an insertion made to maintain the alignment. Stop codons are indicated with a $, and frameshifts by a #, or ambiguous codons (nucleotide was r, y, or n) by an x; they are inserted to maintain the alignments.

D. REFERENCES AND NOTES

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